

Amendment to the Claims

Please cancel claims 5-6, 9-17, 21-24, 26 and 28.

1. (Original) A method of discovering the elements in a compound with a fitness function, comprising:

receiving a set of monoisotopic mass look-up-tables (LUTs) that associates LUT addresses with mass values for a set of elements;

identifying mass values in parallel by cross-referencing two or more LUT addresses associated with an electronic chromosome and addresses in the monoisotopic mass LUTs;

evaluating different permutations of the identified mass values from the set of monoisotopic mass LUTs;

accessing values in two or more mass spectroscopy data sets according to the permutations of mass values identified in the monoisotopic mass LUTs; and

determining the combination of elements in the compound according to a correlation between the permutations of mass values and the mass values associated with the mass spectroscopy data set.

2. (Original) The method of claim 1 wherein evaluating different permutations further comprises:

combining one or more mass values from the set of monoisotopic mass LUTs together; and

adding one or more constant values to the combination of one or more mass values.

3. (Original) The method of claim 1 wherein the compound is a protein and the elements include one or more amino acids to be discovered during protein sequencing analysis.
4. (Original) The method of claim 2 wherein the one or more amino acids are selected from a set of amino acids including: Gly, Ala, Ser, Pro, Val, Thr, Cys, Ile, Leu, Asn, Asp, Gln, Glu, Met, His, Phe, Arg, Tyr, Trp and Lys.
5. (Cancelled.)
6. (Cancelled.)
7. (Original) The method of claim 1 wherein evaluating different permutations may include one or more of the following: adding or subtracting constants values, summing one or more different mass values.
8. (Original) The method of claim 1 wherein the electronic chromosome is a storage area with a series of addresses corresponding to mass values and potentially the elements in the compound.
9. (Cancelled.)
10. (Cancelled.)
11. (Cancelled.)
12. (Cancelled.)
13. (Cancelled.)
14. (Cancelled.)
15. (Cancelled.)
16. (Cancelled.)
17. (Cancelled.)

18. (Original) A computer program product for discovering the elements in a compound with a fitness function, tangibly stored on a computer-readable medium, comprising instructions operable to cause a programmable processor to:

receive a set of monoisotopic mass look-up-tables (LUTs) that associates LUT addresses with mass values for a set of elements;

identify mass values in parallel by cross-referencing two or more LUT addresses associated with an electronic chromosome and addresses in the monoisotopic mass LUTs;

evaluate different permutations of the identified mass values from the set of monoisotopic mass LUTs;

access values in two or more mass spectroscopy data sets according to the permutations of mass values identified in the monoisotopic mass LUTs; and

determine the combination of elements in the compound according to a correlation between the permutations of mass values and the mass values associated with the mass spectroscopy data set.

19. (Original) The computer program product of claim 18 wherein the compound is a protein and the elements include one or more amino acids to be discovered during protein sequencing analysis.

20. (Original) The computer program product of claim 18 wherein evaluating different permutations may include one or more of the following: adding or subtracting constants values, summing one or more different mass values.

21. (Cancelled.)

22. (Cancelled.)

23. (Cancelled.)

24. (Cancelled.)

25. (Original) An apparatus for discovering the elements in a compound with a fitness function, comprising:

a set of monoisotopic mass look-up-tables (LUTs) that associates LUT addresses with mass values for a set of elements;

a set of registers operatively connected to the set of monoisotopic mass LUTs that identifies mass values in parallel by cross-referencing two or more LUT addresses associated with an electronic chromosome and addresses in the monoisotopic mass LUTs;

arithmetic logic that evaluates different permutations of the identified mass values from the set of monoisotopic mass LUTs;

storage driven by arithmetic logic to access values in two or more mass spectroscopy data sets according to the permutations of mass values identified in the monoisotopic mass LUTs; and

arithmetic logic that determines the combination of elements in the compound according to a correlation between the permutations of mass values and the mass values associated with the mass spectroscopy data set.

26. (Cancelled.)

27. (Original) An apparatus for discovering the elements in a compound with a fitness function, comprising:

means for receiving a set of monoisotopic mass look-up-tables (LUTs) that associates LUT addresses with mass values for a set of elements;

means for identifying mass values in parallel by cross-referencing two or more LUT addresses associated with an electronic chromosome and addresses in the monoisotopic mass LUTs;

means for evaluating different permutations of the identified mass values from the set of monoisotopic mass LUTs;

means for accessing values in two or more mass spectroscopy data sets according to the permutations of mass values identified in the monoisotopic mass LUTs; and

means for determining the combination of elements in the compound according to a correlation between the permutations of mass values and the mass values associated with the mass spectroscopy data set.

28. (Cancelled.)